

SEQUENCE LISTING

<110> HOOD, John
ELICEIRI, Brian
CHERESH, David

<120> Methods and Compositions Useful for Modulation of
Angiogenesis Using Tyrosine Kinase Raf and Ras

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<150> US 60/148,924

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7/20

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Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
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NOTED FOR 2013

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Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly Lys Leu	
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Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn	
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Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys	
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Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu	
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gat tgg aat act gat gct gcg tct ttg att gga gaa gaa ctt caa gta	384
Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val	
115 120 125	
gat ttc ctg gat cat gtt ccc ctc aca aca cac aac ttt gct cgg aag	432
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acg ttc ctg aag ctt gcc ttc tgt gac atc tgt cag aaa ttc ctg ctc	480
Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe Leu Leu	
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Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile Arg Gln	
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Sub
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 Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe Thr Phe
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 Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg Gln Arg
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tcg aca tcc aca cct aat gtc cac atg gtc agc acc acg ctg cct gtg 816
 Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu Pro Val
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 Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu Ser Ala
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gta tct ggg acc cag gag aaa aac aaa att agg cct cgt gga cag aga 1008
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 His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro
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 Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr
 385 390 395 400

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ctg gca att gtg acc cag tgg tgc gag ggc agc agc ctc tac aaa cac 1296
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gcc cgg cag acg gct cag gga atg gac tat ttg cat gca aag aac atc 1392
 Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile
 450 455 460

atc cat aga gac atg aaa tcc aac aat ata ttt ctc cat gaa ggc tta 1440
 Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu Gly Leu
 465 470 475 480

aca gtg aaa att gga gat ttt ggt ttg gca aca gta aag tca cgc tgg 1488
 Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser Arg Trp
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agt ggt tct cag cag gtt gaa caa cct act ggc tct gtc ctc tgg atg 1536
 Ser Gly Ser Gln Val Glu Gln Pro Thr Gly Ser Val Leu Trp Met
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gcc cca gag gtg atc cga atg cag gat aac aac cca ttc agt ttc cag 1584
 Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser Phe Gln
 515 520 525

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 Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly
 530 535 540

gag ctt cct tat tct cac atc aac aac cga gat cag atc atc ttc atg 1680
 Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met
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 Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr Lys Asn
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tgc ccc aaa gca atg aag agg ctg gta gct gac tgt gtg aag aaa gta 1776
 Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
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aag gaa gag agg cct ctt ttt ccc cag atc ctg tct tcc att gag ctg 1824
 Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu

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See
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595 600 605

ctc caa cac tct cta ccg aag atc aac cgg agc gct tcc gag cca tcc 1872
 Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu Pro Ser
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ttg cat cgg gca gcc cac act gag gat atc aat gct tgc acg ctg acc 1920
 Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr Leu Thr
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acg tcc ccg agg ctg cct gtc ttc tac tcg ttc ctg ccg ttc ttc ttc 1968
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Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp
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Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys
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Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu
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Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val
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Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala Arg Lys
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Sub
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 195 200 205
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 210 215 220
 Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe Thr Phe
 225 230 235 240
 Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg Gln Arg
 245 250 255
 Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu Pro Val
 260 265 270
 Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu Ser Ala
 275 280 285
 Ser Pro Ser Ala Leu Ser Ser Ser Pro Asn Asn Leu Ser Pro Thr Gly
 290 295 300
 Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro
 305 310 315 320
 Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg
 325 330 335
 Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met Leu Ser
 340 345 350
 Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp
 355 360 365
 His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro
 370 375 380
 Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr
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 Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys Asp Asn
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Sub
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cont

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